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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/751,962

DATE: 01/24/2002 TIME: 18:46:52

Input Set: N:\Crf3\RULE60\09751962.raw
Output Set: N:\CRF3\01242002\1751962.raw

SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
             (i) APPLICANT: CATCHESIDE; DAVID E.
            (ii) TITLE OF INVENTION: REAGENTS AND METHODS FOR DIVERSIFICATION
      7
                                      OF DNA
      8
           (iii) NUMBER OF SEQUENCES: 2
     10
            (iv) CORRESPONDENCE ADDRESS:
     12
     13
                  (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
                  (B) STREET: 3100 Norwest Center, 90 South 7th Street
     14
                  (C) CITY: Minneapolis
     15
                  (D) STATE: MN
                                                     ENTERED
     16
                  (E) COUNTRY: USA
     17
                  (F) ZIP: 55402
     18
             (V) COMPUTER READABLE FORM:
     20
     21
                  (A) MEDIUM TYPE: Diskette
                  (B) COMPUTER: IBM Compatible
     22
     23
                  (C) OPERATING SYSTEM: DOS
                  (D) SOFTWARE: FastSEQ for Windows Version 2.0
     24
            (vi) CURRENT APPLICATION DATA:
     26
C--> 27
                  (A) APPLICATION NUMBER: US/09/751,962
C--> 28
                  (B) FILING DATE: 29-Dec-2000
     29
                  (C) CLASSIFICATION:
     31
           (vii) PRIOR APPLICATION DATA:
     32
                  (A) APPLICATION NUMBER: 08/977,171
     33
                  (B) FILING DATE:
     37
          (viii) ATTORNEY/AGENT INFORMATION:
     38
                  (A) NAME: Skoog, Mark T
     39
                  (B) REGISTRATION NUMBER: 40,178
                  (C) REFERENCE/DOCKET NUMBER: 10552.13US01
     40
     42
            (ix) TELECOMMUNICATION INFORMATION:
     43
                  (A) TELEPHONE: 612-332-5300
     44
                  (B) TELEFAX: 612-332-9081
     45
                  (C) TELEX:
     49 (2) INFORMATION FOR SEQ ID NO: 1:
     51
             (i) SEQUENCE CHARACTERISTICS:
     52
                  (A) LENGTH: 9775 base pairs
     53
                  (B) TYPE: nucleic acid
     54
                  (C) STRANDEDNESS: single
     55
                  (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: Genomic DNA
     57
     59
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                 60
         GATCGCAACT GGAGATCACT CGCACCGTGC CGCAGAACAA GGGCGACGAG CCTCAGGGCA
     61
                                                                                120
         GTTTAGCCTG CCGTAACAGC ACAGACCATA GCTTATTTTC ACCTGGGCGG GCGGGCGACG
```

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63	GCGGCACTGA	CATCGGCAAG	GCGGCATCAA	GCAACCCCTC	TGTTGCTTGC	CAGCTGCCGG	180
64	CCAACGTCAG	CGGTACAAGG	AGAAATCTGG	AAGGAAAGAC	TTCTGGCACC	GACAGGATGG	240
65	CACGCGGGAA	AAGTTCCCAA	TGCATGAGAT	GAGGGGCATT	TGCATTGCCT	CCCGTCACAC	300
66	TGCCCGCGAA	CCCCAACCCC	ACCATAGCGT	CTGTCGATAC	ATGGAGCGCG	AAGTCGAGAA	360
67	ACCTGTAATT	CCTGGTAACT	TTCAGGTACA	CAGTACGTAC	TGATCCTGGT	ATCAAACCTT	420
68	GCCTGCCGAG	TTTTCGACGG	AAAGAGGTGT	GAATTGTGAA	AGAGTCATAC	CAAATCACCC	480
69	GATTTTCATA	AAGCCCGAGT	CTTTTCTGTA	CATAAGCGAC	ACTCGAAGCG	GGCCTCATCT	540
70	TCATAGCCTG	ATAGCTTGTA	ATACTCCATC	CTCGTATCTC	ACTTGACCTT	GAGTTCAACC	600
71	CCACGTCAGA	CTTCACCCGA	CACATCGACG	GATTGGGGAA	CAGCACAATA	CCTGAAAAGC	660
72	GAGAAAACCA	AACAGAGGAA	AACACCATGG	AGACAACACT	TCCCCTCCCC	TTCCTCGTCG	720
73	GTGTCAGTGT	TCCTCCCGGA	CTGAATGACA	TCAAGGAGGG	CCTCAGCCGG	GAGGAAGTCT	780
74	CGTGTCTTGG	CTGCGTCTTC	TTCGAGGTCA	AGCCCAAGAC	CCTTGAGAAA	ATCGTGCGAT	840
75				CCTACTTCGA			900
76				GCGCCCGCAA			960
77				GCGTTGCCCC			1020
78				GCCTTTTGCT			1080
79				CCAGAGACAA			1140
80				AGTTCATCCA			1200
81				CAACAAAGAA			1260
82				AGTCTGACCG			1320
83				TGGGTCTGGT			1380
84				TCTATCAGAG			1440
85				AGCTCGTCCG			1500
86				AGGGTCGTTT			1560
87				AGCTCGAGCA			1620
88				GTCTCTTCTC			1680
89				GCACCGCTCA			1740
				TTACCAGGGC			1800
90				AGAGCTGGAA			1860
91				GCATCAAGCC			1920
92							1920
93				CCCAGGAGAC			
.94				CCGAGGAGCT			2040
95				AGATCATTGT			2100
96				ACACTCACAA			2160
97				CCAAGGAGCT			2220
98				ACATCCGCAA			2280
99				CCGGTGTTGT			2340
100			-			AGCACTGCCC	2400
101						GCCTCTCCTC	2460
102						GTTGGGGCCG	2520
103						GGCACCGAGA	2580
104						GCTGCCAAGA	2640
105						GGCCCGTCCG	2700
106						GATCTCCTGT	2760
107						CTCGACGAGG	2820
108						CCTCGCGTCC	2880
109						GTCGAGGAGG	2940
110	CCATGGAGCT	CAGCAACAAG	TACGCTCCTC	AGCACTTGAT	CCTCCAGATO	AAGGAGGCCG	3000
111	AGAAAGCTGI	CGATCTTGTC	ATGAACGCTG	GTAGTGTCTT	CATTGGCGCI	TGGACTCCTG	3060

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112				ACCACTCGCT			3120
113				CGTCAAGACA			3180
114	GCAAGCAGTA	CTCTGGCGTC	AATCTCGCCT	CGTTCGTCAA	GCACATTACC	AGCTCCAACT	3240
115				AGGCTGTCAT			3300
116	AGCTCGAGGC	TCACAGAAGG	GCGGTCAGCA	TCCGTCTTGA	GCACATGAGC	AAGAGCAACT	3360
117	AGACGGAAAT	TCTTTTTCGA	AGTTGCAAAA	AAAACAAGAA	CAAAAGGATG	TAGTGGGTTG	3420
118	ATGTATATCT	GGGTCATTTT	GGGCACATAG	AGTAATGATA	ACGAGTTTTG	GACATTGTAC	3480
119	TGTTCTGTAC	AGGCTGAAGA	TCAGTACATG	AATCTGTTGG	TAAGTGTAGA	GACCCAAACG	3540
120	TCCCTTGAGT	TTTTCTCCCT	GTTCCAGAGA	GGTGCTCGTC	CCTGGGTGTT	TATTTTCATT	3600
121	ATTACATCAA	CCTTTTATTT	TATTTTATTT	TTTATTTTAC	TTTTTTTCC	TTTTTTTCAG	3660
122	ATCATGCGTA	CATGAACGGG	GGAAGCACAG	ACGATCGAAA	CGTGGATGTC	ACAATGTCGC	3720
123	TGCAGTGATG	CTGCATTGCA	TGAAGCGCCC	ATCTCAATAT	ACTTGCAGTC	TTGCGCGTTG	3780
124	CACGTGAACT	TCCCAAACAA	CCGAATAAAA	GACGGCGAAA	AATGAAGATA	AAAAAAAACC	3840
125	ATAATAAAA	TCGGAGGGAG	TGTGGGAAAT	GGTTTCTTTT	AGCATTTAGA	CCCCATAGCC	3900
126	GTGCACGCCC	GGGTACAGAC	AGGTTCATCG	ATGTTGACAT	TGACTGGGAC	ACCAGGTCTA	3960
127	TCTATTTCAT	CTCCTGTCCT	CTACCATACA	TCGGGACATC	GGACATCTCG	CTGTACCCCC	4020
128	CACACCCACA	AAGTCTTATA	AAAGCGCCAC	ACCCGAGGAG	GTTCGGTCGG	CCCCACGAAC	4080
129	TCCGTGCCTC	CCTGCCTGTT	TACAGGGACC	GAACGCTGGA	GAAGCTTAGT	TTCCTGACAT	4140
130				TCATAGGCGA			4200
131				GGTACTGTAT			4260
132	TCTTGGCTGG	GACATTGTTA	ATACCTCGAT	ATGATGAAGT	GGGAGGGAGT	TTTTTCATGT	4320
133				TTTTGTACCA			4380
134				TCTGAGGATC	and the second s		4440
135				GCGAGCGGTC			4500
136						TAGTAGTACA	4560
137				TTGCTATTCA			4620
138				TATGGAAAAA			4680
139				GTCAGAATGC			4740
140						CAAGCTACCC	4800
141				TCAGGTGTTT			4860
142				ATTAGACCAT			4920
143				GACTTGAGAG			4980
144				CTAACCGACG			5040
145				TTTGGCCGGA			5100
146				GGTAGGTGTC			5160
147				ATGAGTTGTA			5220
148				TTCTCGTCTT			5280
149				AACATGAGAA			5340
150				TGAGGATAGG			5400
151				CAGCAAACTG			5460
152				AGCCTTGGTA			5520
153				GGGAGGATCT			5580
154				TGTTAGGCTT			5640
155				TAGACTTACT			5700
156				GACTTTGCTT			5760
157				GGCTCTTTTT			5820
158				CAAGGTAGGT			5880
159				GTCATGATGA			5940
160				CAGTGGTTGT			6000
100	TOOTINCOOR	GAGCIGGAC	CGCIMGGCCT	CHGIGGIIGI	GCCATICAGC	0100010101	

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161	GGAGTAGCGG	TAGAGGCGCT	TGGAAGTTGT	GCTAGCGGAA	ACCCTGGAAT	ATCTTGTACC	6060
162	CTTCGATTCC	TTCTCGGGCT	GCCCATGTGC	TGAGGTGATG	CCGGGGATCT	GGCGCCAATC	6120
163	ATCCATTGAG	GTTCCCGCAG	CTTCCCGGTG	CCGCGCGCGG	GCGCAGTTGC	TCACAGGACA	6180
164	CACCTAGACG	CAGGGGCACA	GGGGCACCGT	TTGGTGTGCA	ACTGGGTACC	TGGTAGCTGT	6240
165	AGCAAGCACT	CCACCGTCTG	TGCAATCCCC	CAATCCACGG	CAGGAACTTA	GCACCGCCGC	6300
166	GGCACCGAGT	GAGCGAATCC	ATCCGCATTG	GATCCCAATT	CTTGCCCTTG	CCATCCTTCT	6360
167	TTCTTCCCAC	TTGGCGCAAC	CAACACTTCC	CTTGGTCTGG	GTACTCGTGT	TGATCTTCAC	6420
168	TCTCTTTTTT	TCTTGGGCGA	CCGACTTTTT	ATATCCGTCC	TTGCTTCCCC	CTGGCCGTTG	6480
169					CTTGGTTCGG		6540
170	AAAAACAGAA	CAATTCCGGC	TCTTCCAGGT	GGCTTGGGTG	CGACTGTTTA	GCTCTTGACC	6600
171	ACTAGCCGCT	TACCTTCTCT	TGATGTTTAT	ATTTGGATAT	CATTGAACTA	CTCTTTCTTG	6660
172					GATATACGTT		6720
173					ATCGTCGCTG		6780
174					ACCCCAACGC		6840
175					CGAATTCGCC		6900
176					CGCTCCGGAA		6960
177					AGAACACCAT		7020
178					CCGAAACTTT		7080
179					CCATTTCAGG		7140
180					ATAACCGGAT		7200
181						TGTAAAACCA	7260
182						TTCGACGTTG	7320
183					TCCATGCCCC		7380
184					AAAAAAAAA		7440
185					CTTTCTGGTG		7500
186					ACCCTGCTGA		7560
187					GAGGCTGGCC		7620
188					GCGAAGAAGA		7680
189					AGTTACCAAC		7740
190						ACTTCCAGAA	7800
191					GCGCCTGGAG		7860
192					ACGGGTAGCT		7920
193					TTCAGCAACG		7980
194					TTCGTCATGG		8040
195					TACGACGGTG		8100
196					CGCCAAGAGG		8160
197					ACCAACCCCA		8220
198	GCTCGAGCTC	GACCTGGTCG	ACGGCGGCGA	AGATCTGCAG	AATATTCCGC	TCAACCCGCT	8280
199					GACTCGTCCG		8340
200					CGCACTTTCG		8400
201					TTTATAAACC		8460
202					ACCTTGAACG		8520
203					ACCGCGCTGA		8580
204	CACCTTCGAT	CCGTCATACA	CGATGTCTCA	GCGCAACGAC	ATCATCGGCA	ACGGATGGAA	8640
205					CCCACTTGCG		8700
206					CCAGCCGCGT		8760
207					GATACGGGGG		8820 8880
208					GCTGTTGCTA		8940
209	GGTGAATGTC	TGGTCGTCGG	TTGTGGTGGG	AGTTGTGGCG	GCTACTTTGT	TGTTGTAGGG	0940

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-	210	GTAGGGGAGA	CGTGATGATA	TTCCAGTCTG	ATGAAGTTGA	GACTGGACTG	GAGATCGCCA	9000
	211					ATGGATGAAG		9060
	212					CACACTGCAT		9120
	213	ттсатастат	GCTTTGGCAT	TTACGTTTAA	CAATCAATTG	CTCCATCCTG	ATGTTCTATC	9180
	214	TTTTTTCGACA	ATGGATTGAT	ACTACTCCTG	TTGCTTCGCT	CTTGAGGTTG	GAAGGACTTG	9240
	215					ATCGAAGTAT		9300
	216					ACGGTCGGAT		9360
	217					TGCCCACACC		9420
	218					CCTTTCCATC		9480
	219					TTCTCCTTTG		9540
	220					TCACTCAAAC		9600
	221					TTCTTACGAC		9660
	221	CAICGAAGAA	TOTAL CATTO	TCA ACCCTCT	CCTCCACTTC	GATCTGTTTA	ACTTCCGCAG	9720
						AAAAAAAAA		9775
	223	(2) INFORMAT			TICCAMAMA	AAAAAAAAAA	ATTAC	3113
							•	
		(i) SE(:	
	229	•	A) LENGTH: S	_	alls		•	
	230		B) TYPE: nuc		_			
	231		C) STRANDED		=			
	232		TOPOLOGY:		13			
	234		LECULE TYPE:					
	236	(X1) SE(QUENCE DESCI	CHARCECCAA	COCCCCCAC	GGGTCACTGA	CCCAATCCAC	60
	238							120
	239					GTAGTAGATC		180
	240	ATCACTCGCA	CCGTGCCGCA	GAACAAGGGC	GACGAGCCTC	AGGGCAGTTT	CACTICACATIC	240
	241					GCGACGCGA		300
	242					TGCCGGCCAA		360
	243					GGATGGCACG		420
	244					TCACCCAGTG		480
	245					AGAAACCTGT		540
	246					CCTTGCCTGC		600
	247					ACCCGATTTT		660
	248					ATCTTCATAG		
	249					AACCCCACGT		720
	250					AAGCGAGAAA		780
	251					GTCGGTGTCA		8 4 0 900
	252					GTCTCGTGTC		
	253						AGCGTCACAA	960
	254					TCTATCGATG		1020
	255	TCTTCTGGAC	GCCGGCGCCC	GCAAGGTGTT	TGTCAAGACC	GAGCAGTTGG	CCGACCTCTC	1080
	256	CGCATATGGC	TCCCGCGTTG	CCCCCATTGT	CACTGGAAGC	AGCGCTGCTT	TGCTTTCCTC	1140
	257	CGCCACCGAG	AGCGGCCTTT	TGCTCTCCGG	CTTCGATCAG	ACTGCCTCCG	AGGCTGCACA	1200
	258					TTCATCAAGC		1260
	259					AACGCCATCC		1320
	260	ATCCACTGGC	TTGACAACAA	AGAAGGACGA	GGCCGGCAAG	CTTGCCATCT	CCACCATCCT	1380
	261	CTCGAGCGTC	TGGAAGTCTG	ACCGTCCCGA	TGGTCTTCTC	CCCACCGTTG	TCGTTGATGA	1440
	262					AGTGTGAACG		1500
	263					TGGTACAAGG		1560
2	264	CGGAGACACT	CAGGAGCTCG	TCCGCATCTC	GCTTGACTGC	GATAACGATG	CTCTCAAGTT	1620

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2